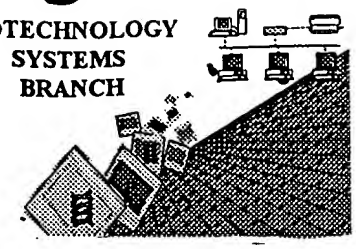
BIOTECHNOLOGY SYSTEMS BRANCH



#6

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/914,454 A
Source: PCTO9
Date Processed by STIC: 6/12/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**>, **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
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4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/914,454

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2____Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3_✓_Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4____Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5____Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6____PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7____Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8____Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9____Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10____Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11____Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12____PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13____Misuse of n	n can only be used to represent a single **nucleotide** in a nucleic acid sequence. N is **not** used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING DATE: 07/05/2002
PATENT APPLICATION: US/09/914,454A TIME: 15:39:27

Input Set : N:\Crf3\06122002\I914454.raw
Output Set: N:\CRF3\07052002\I914454A.raw

Does Not Comply
Corrected Diskette Needed

delete multiple <110>'s only one is needed

```
     1 <110> APPLICANT: Chiron SpA
W--> 2 <110> APPLICANT: GRANDI Guido
W--> 3 <110> APPLICANT: RAPPUOLI Rino
W--> 4 <110> APPLICANT: GIULIANI Marzia Monica
W--> 5 <110> APPLICANT: PIZZA Mariagrazia
     6 <120> TITLE OF INVENTION: ENHANCEMENT OF BACTERICIDAL ACTIVITY OF NEISSERIA ANTIGENS
WITH
     7       OLIGONUCLEOTIDES CONTAINING CG MOTIFS
     8 <130> FILE REFERENCE: P023888WO
     9 <140> CURRENT APPLICATION NUMBER: US/09/914,454A
    10 <141> CURRENT FILING DATE: 2002-03-22
    11 <150> PRIOR APPLICATION NUMBER: US-60/121,792
W--> 12 <151> PRIOR FILING DATE: 26/02/1999
    13 <160> NUMBER OF SEQ ID NOS: 34
    14 <170> SOFTWARE: SeqWin99
```

1999-02-26 G use this format for dates

ERRORED SEQUENCES

```
   304 <210> SEQ ID NO: 31
   305 <211> LENGTH: 442
   306 <212> TYPE: PRT
   307 <213> ORGANISM: Neisseria meningitidis
   308 <400> SEQUENCE: 31
   309       Met Lys Lys Tyr Leu Phe Arg Ala Ala Leu Tyr Gly Ile Ala Ala Ala
   310       1               5                   10                  15
   311       Ile Leu Ala Ala Cys Gln Ser Lys Ser Ile Gln Thr Phe Pro Gln Pro
   312                   20                  25                  30
   313       Asp Thr Ser Val Ile Asn Gly Pro Asp Arg Pro Val Gly Ile Pro Asp
   314               35                  40                  45
   315       Pro Ala Gly Thr Thr Val Gly Gly Gly Gly Ala Val Tyr Thr Val Val
   316           50                  55                  60
   317       Pro His Leu Ser Leu Pro His Trp Ala Ala Gln Asp Phe Ala Lys Ser
   318       65                  70                  75                  80
   319       Leu Gln Ser Phe Arg Leu Gly Cys Ala Asn Leu Lys Asn Arg Gln Gly
   320                   85                  90                  95
   321       Trp Gln Asp Val Cys Ala Gln Ala Phe Gln Thr Pro Val His Ser Phe
   322                   100                 105                 110
   323       Gln Ala Lys Gln Phe Phe Glu Arg Tyr Phe Thr Pro Trp Gln Val Ala
   324               115                 120                 125
   325       Gly Asn Gly Ser Leu Ala Gly Thr Val Thr Gly Tyr Tyr Glu Pro Val
   326           130                 135                 140
   327       Leu Lys Gly Asp Asp Arg Arg Thr Ala Gln Ala Arg Phe Pro Ile Tyr
   328       145                 150                 155                 160
```

441 shown (p. 2)

RAW SEQUENCE LISTING DATE: 07/05/2002
PATENT APPLICATION: US/09/914,454A TIME: 15:39:27

Input Set : N:\Crf3\06122002\I914454.raw
Output Set: N:\CRF3\07052002\I914454A.raw

```
329       Gly Ile Pro Asp Asp Phe Ile Ser Val Pro Leu Pro Ala Gly Leu Arg
330                       165                 170                 175
331       Ser Gly Lys Ala Leu Val Arg Ile Arg Gln Thr Gly Lys Asn Ser Gly
332                   180                 185                 190
333       Thr Ile Asp Asn Thr Gly Gly Thr His Thr Ala Asp Leu Ser Arg Phe
334               195                 200                 205
335       Pro Ile Thr Ala Arg Thr Thr Ala Ile Lys Gly Arg Phe Glu Gly Ser
336           210                 215                 220
337       Arg Phe Leu Pro Tyr His Thr Arg Asn Gln Ile Asn Gly Gly Ala Leu
338       225                 230                 235                 240
339       Asp Gly Lys Ala Pro Ile Leu Gly Tyr Ala Glu Asp Pro Val Glu Leu
340                       245                 250                 255
341       Phe Phe Met His Ile Gln Gly Ser Gly Arg Leu Lys Thr Pro Ser Gly
342                   260                 265                 270
343       Lys Tyr Ile Arg Ile Gly Tyr Ala Asp Lys Asn Glu His Pro Tyr Val
344               275                 280                 285
345       Ser Ile Gly Arg Tyr Met Ala Asp Lys Gly Tyr Leu Lys Leu Gly Gln
346           290                 295                 300
347       Thr Ser Met Gln Gly Ile Lys Ser Tyr Met Arg Gln Asn Pro Gln Arg
348       305                 310                 315                 320
349       Leu Ala Glu Val Leu Gly Gln Asn Pro Ser Tyr Ile Phe Phe Arg Glu
350                       325                 330                 335
351       Leu Ala Gly Ser Ser Asn Asp Gly Pro Val Gly Ala Leu Gly Thr Pro
352                   340                 345                 350
353       Leu Met Gly Glu Tyr Ala Gly Ala Val Asp Arg His Tyr Ile Thr Leu
354               355                 360                 365
355       Gly Ala Pro Leu Phe Val Ala Thr Ala His Pro Val Thr Arg Lys Ala
356           370                 375                 380
357       Leu Asn Arg Leu Ile Met Ala Gln Asp Thr Gly Ser Ala Ile Asp Gly
358       385                 390                 395                 400
359       Ala Val Arg Val Asp Tyr Phe Trp Gly Tyr Gly Asp Glu Ala Gly Glu
360                       405                 410                 415
361       Leu Ala Gly Lys Gln Lys Thr Thr Gly Tyr Val Trp Gln Leu Leu
362                   420                 425                 430
363       Pro Asn Gly Met Lys Pro Glu Tyr Arg Pro
E--> 364          ~~435~~ 435             ~~440~~ 440
```

misaligned amino acid numbering - see item 3 on Error Summary Sheet

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/05/2002
PATENT APPLICATION: US/09/914,454A TIME: 15:39:28

Input Set : N:\Crf3\06122002\I914454.raw
Output Set: N:\CRF3\07052002\I914454A.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

VERIFICATION SUMMARY DATE: 07/05/2002
PATENT APPLICATION: US/09/914,454A TIME: 15:39:28

Input Set : N:\Crf3\06122002\I914454.raw
Output Set: N:\CRF3\07052002\I914454A.raw

L:2 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:3 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:4 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:5 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:364 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
L:364 M:252 E: No. of Seq. differs, <211> LENGTH:Input:442 Found:441 SEQ:31